

## SEQUENCE LISTING

<110> Duncan, Roy  
<120> NOVEL REOVIRUS-DERIVED PROTEINS AND USES THEREFOR  
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10 <140> 08/965,708  
<141> 1997-11-07  
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Asn Gly Ala Thr Ala Val Phe Gly Asn Val His Cys Gln Ala Ala Gln  
10 15 20 25  
  
50 aac acg gca ggt ggt gat ttg caa gct acg tca tcc ata att gca tat 147  
Asn Thr Ala Gly Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr  
30 35 40  
  
tgg cct tat cta gcg gcg ggt ggt ttc tta tta att gtt atc att 195  
Trp Pro Tyr Leu Ala Ala Gly Gly Phe Leu Leu Ile Val Ile Ile  
45 50 55  
  
ttc gct ctt cta tac tgt tgt aag gct aag gtc aag gcg gac gct gca 243  
Phe Ala Leu Leu Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala  
60 65 70  
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291

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| cgt agt gtc ttc cat cgt gag ctg gta gcg ttg agt tct ggt aag cac    |      |
| Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His    |      |
| 75   | 80   |
| 85   |      |
| aat gca atg gct ccg cca tac gac gtt tgaagtgc aa cgatttaatt         | 338  |
| Asn Ala Met Ala Pro Pro Tyr Asp Val                                |      |
| 90   | 95   |
| tctgtccgct atcaacttcgc gaacttgcta tcccatcatt tactgctata actggggctg | 398  |
| accatcaca gtatTTAAC attgagctcc cacacactca tcctctctat tccaaattgc    | 458  |
| ctactctgtt atctcaaccc ttgtagggtcc acgtgcggct gattgcggg ttcgctct    | 518  |
| attcaacatt gtcaagtatt ttgtagatcg attgtgctt actattctcc ccacacgcta   | 578  |
| tcgttccatt gcgtgcattt gatcggcggt cttgtcttat agttcattgg gatggcggt   | 638  |
| ctcaatccat cgcagcgaag agaggtcgac agcttgatc ttgtcattgac ttgcacgtg   | 698  |
| actataagtc atggcgattt gacgcgcgatc tatgaacggc tgaccaatct agaagcgtct | 758  |
| acggagttt tacatcgctc cattttcgat atatccacta ctgtctcaa tatttctgca    | 818  |
| aatttacaag acatgaccca taccttggat gatgtactg ctaatttaga cggtttgagg   | 878  |
| accactgtta ctgcacttca ggattccgtc tccattctgt ctacaaatgt gactgactt   | 938  |
| acgaacacat cctctgcgca cgcggcgaca ctatcttac ttcaaactac ggttgacgga   | 998  |
| aactccactg ccatctccaa tttgaagagt gatgtatcg cgaacggttt agctattaca   | 1058 |
| gatctgcagg atcgtttaa atcattggag tctaccgcga gtcatggct atcttttcg     | 1118 |
| cctccgctt gtgtcgctga cggcggtt tcattagaca tggacccccta cttctgttct    | 1178 |
| caacgagttt cttaacatc atactcgccg gaggctcaac taatgcaatt tcggtgatg    | 1238 |
| gcacggggta ctaacggatc atctgatacc attgacatga ccgttaacgc tcactgtcat  | 1298 |
| ggaagacgca ctgattat gatgtcgcc acggaaatc tcacggcac tagtaacgtc       | 1358 |
| gtgttattaa cttcgattt aagtgacata acgcataatcc catcagaccc agcacgtctt  | 1418 |
| gttcccagtg cgggatttca agctgcgtcg ttccctgtgg acgtatcatt caccgcgat   | 1478 |
| tctgcactc atgcgtacca agcgtatggg gtgtactcga gctcacgtt cttcacaatt    | 1538 |
| actttccaa cccggaggta tggtacagcg aacattcggtt ccttgaccgt gcgtaccggc  | 1598 |
| atcgacacct aagggtgtggc gccgtactgg gattggttat tcata                 | 1643 |

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<210> 2  
<211> 98  
<212> PRT  
<213> avian reovirus strain 176

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| 10  |    |
| 15  |    |
| Gly Asn Val His Cys Gln Ala Ala Gln Asn Thr Ala Gly Gly Asp Leu |    |
| 20  | 25 |
| 30  |    |
| Gln Ala Thr Ser Ser Ile Ile Ala Tyr Trp Pro Tyr Leu Ala Ala Gly |    |
| 35  | 40 |
| 45  |    |
| Gly Gly Phe Leu Leu Ile Val Ile Ile Phe Ala Leu Leu Tyr Cys Cys |    |
| 50  | 55 |
| 60  |    |
| Lys Ala Lys Val Lys Ala Asp Ala Ala Arg Ser Val Phe His Arg Glu |    |
| 65  | 70 |
| 75  |    |
| 80  |    |
| Leu Val Ala Leu Ser Ser Gly Lys His Asn Ala Met Ala Pro Pro Tyr |    |
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| Asp Val   |    |

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Cys Pro Leu Ser Leu Arg Glu Leu Ala Ile Pro Ser Phe Thr Ala Ile  
20 25 30  
10 Thr Gly Ala Asp Pro Ser Gln Tyr Phe Asn Ile Glu Leu Pro His Thr  
35 40 45  
His Pro Leu Tyr Ser Lys Leu Pro Thr Leu Leu Ser Gln Pro Cys Arg  
50 55 60  
Val His Val Arg Leu Ile Arg Arg Phe Ala Leu Tyr Ser Thr Leu Ser  
65 70 75 80  
20 Ser Ile Cys Glu Tyr Asp Cys Ala Leu Leu Phe Ser Pro His Ala Ile  
85 90 95  
9 Val Pro Leu Pro Ala Ser Asp Arg Arg Ser Cys Leu Ile Val His Trp  
100 105 110  
Asp Gly Gly Ser Gln Ser Ile Ala Ala Lys Arg Gly Arg Gln Leu Asp  
115 120 125  
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35 Asp Leu  
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<213> avian reovirus strain 176  
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20 25 30  
Ile Tyr Glu Arg Leu Thr Asn Leu Glu Ala Ser Thr Glu Leu Leu His  
35 40 45  
50 Arg Ser Ile Ser Asp Ile Ser Thr Thr Val Ser Asn Ile Ser Ala Asn  
50 55 60  
Leu Gln Asp Met Thr His Thr Leu Asp Asp Val Thr Ala Asn Leu Asp  
65 70 75 80  
Gly Leu Arg Thr Thr Val Thr Ala Leu Gln Asp Ser Val Ser Ile Leu  
85 90 95  
60 Ser Thr Asn Val Thr Asp Leu Thr Asn Thr Ser Ser Ala His Ala Ala  
100 105 110

Thr Leu Ser Ser Leu Gln Thr Thr Val Asp Gly Asn Ser Thr Ala Ile  
 115 120 125

Ser Asn Leu Lys Ser Asp Val Ser Ser Asn Gly Leu Ala Ile Thr Asp  
 130 135 140

Leu Gln Asp Arg Val Lys Ser Leu Glu Ser Thr Ala Ser His Gly Leu  
 145 150 155 160

10 Ser Phe Ser Pro Pro Leu Ser Val Ala Asp Gly Val Val Ser Leu Asp  
 165 170 175

Met Asp Pro Tyr Phe Cys Ser Gln Arg Val Ser Leu Thr Ser Tyr Ser  
 180 185 190

Ala Glu Ala Gln Leu Met Gln Phe Arg Trp Met Ala Arg Gly Thr Asn  
 195 200 205

Gly Ser Ser Asp Thr Ile Asp Met Thr Val Asn Ala His Cys His Gly  
 210 215 220

Arg Arg Thr Asp Tyr Met Met Ser Ser Thr Gly Asn Leu Thr Val Thr  
 225 230 235 240

Ser Asn Val Val Leu Leu Thr Phe Asp Leu Ser Asp Ile Thr His Ile  
 245 250 255

Pro Ser Asp Leu Ala Arg Leu Val Pro Ser Ala Gly Phe Gln Ala Ala  
 260 265 270

30 Ser Phe Pro Val Asp Val Ser Phe Thr Arg Asp Ser Ala Thr His Ala  
 275 280 285

Tyr Gln Ala Tyr Gly Val Tyr Ser Ser Ser Arg Val Phe Thr Ile Thr  
 290 295 300

Phe Pro Thr Gly Gly Asp Gly Thr Ala Asn Ile Arg Ser Leu Thr Val  
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40 Arg Thr Gly Ile Asp Thr  
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<210> 5  
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60 <220>  
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aac ggt gca aca gct atc ttt ggt aac gtc cat tgt cag gcg gct caa 99  
 Asn Gly Ala Thr Ala Ile Phe Gly Asn Val His Cys Gln Ala Ala Gln  
 10 15 20 25

10 aat act gcc ggc ggc gac ttg caa gct acc tca tcc ata att gcc tat 147  
 Asn Thr Ala Gly Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr  
 30 35 40

tgg cct tat cta gcg gcg ggt ggt ttt ttg ttg att att att att 195  
 Trp Pro Tyr Leu Ala Ala Gly Gly Phe Leu Leu Ile Ile Ile Ile  
 45 50 55

20 ttt gcc atc ttc tac tgt tgt aag gct aaa gtt aaa gcg gac gct gca 243  
 Phe Ala Ile Phe Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala  
 60 65 70

cgg agt gtt ttc cac cgt gag ctt gta gca ctg agc tct ggt aag cac 291  
 Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His  
 75 80 85

aat gca atg gct ccg cca tac gac gtt tgaagtgc aa cgctttgatt 338  
 Asn Ala Met Ala Pro Pro Tyr Asp Val  
 90 95

30 tctgccaaat atcacttcgt gagcttgcca ccccatcgaa tactgctata attgggattg 398  
 acccatcagtttataat attgagctt cgcacacgca tcctctctac tctaaggttgc 458  
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 aactccacta ccattgataa ttggaaaagt gatgtatcat caaacggctc tgctatcaca 1058  
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Gln Ala Thr Ser Ser Ile Ile Ala Tyr Trp Pro Tyr Leu Ala Ala Gly  
 35 40 45

Gly Gly Phe Leu Leu Ile Ile Ile Phe Ala Ile Phe Tyr Cys Cys  
 50 55 60

10 Lys Ala Lys Val Lys Ala Asp Ala Ala Arg Ser Val Phe His Arg Glu  
 65 70 75 80

Leu Val Ala Leu Ser Ser Gly Lys His Asn Ala Met Ala Pro Pro Tyr  
 85 90 95

Asp Val

20 <210> 7  
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 <213> avian reovirus strain 138

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30 Ile Gly Ile Asp Pro Ser Arg Tyr Phe Asn Ile Glu Leu Ser His Thr  
 35 40 45

His Pro Leu Tyr Ser Lys Leu Pro Thr Leu Leu Ser Gln Pro Cys Arg  
 50 55 60

Val His Val Arg Leu Ile Arg Arg Phe Ala Leu Cys Ser Thr Leu Ser  
 65 70 75 80

40 Ser Ile Cys Glu Tyr Asp Cys Ala Leu Leu Ser Pro His Ala Ile  
 85 90 95

Thr Pro Leu Ser Ser Asp Gln Arg Ser Tyr Leu Ile Val His Trp  
 100 105 110

Asp Gly Gly Ser Gln Ser Ile Thr Ala Lys Arg Gly Arg Gln Leu Asp  
 115 120 125

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 130 135 140

Asn Leu  
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<210> 8  
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 <212> PRT  
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Ile Tyr Glu Arg Leu Thr Ser Leu Glu Ala Ser Ala Glu Ser Leu Tyr  
35 40 45

10 Arg Ser Ile Ser Ser Met Ser Thr Thr Val Ser Asp Ile Ser Ala Asp  
50 55 60

Leu Gln Asn Val Thr Arg Ala Leu Asp Asp Val Thr Ala Asn Leu Asp  
65 70 75 80

Gly Met Arg Val Thr Ile Thr Thr Leu Gln Asp Ser Val Ser Thr Leu  
85 90 95

20 Ser Thr Thr Val Thr Asp Leu Thr Asn Thr Ser Ser Val His Ser Glu  
100 105 110

Ala Leu Ser Ser Leu Arg Thr Ile Val Asp Gly Asn Ser Thr Thr Ile  
115 120 125

Asp Asn Leu Lys Ser Asp Val Ser Ser Asn Gly Leu Ala Ile Thr Asp  
130 135 140

30 Leu Gln Ser Arg Val Lys Ser Leu Glu Ser Val Ser Ser His Gly Leu  
145 150 155 160

Ser Phe Ser Pro Pro Leu Ser Val Ala Asp Asp Val Val Ser Leu Ser  
165 170 175

Met Asp Pro Tyr Phe Cys Ser Gln Arg Val Thr Leu Thr Ser Tyr Ser  
180 185 190

Ala Glu Ala Gln Leu Met Gln Phe Gln Trp Met Ala Arg Gly Ala Asn  
195 200 205

40 Gly Ser Ser Asp Thr Ile Asp Met Thr Val Asn Ala His Cys His Gly  
210 215 220

Arg Arg Thr Asp Tyr Ile Met Ser Ser Thr Gly Gly Leu Thr Val Thr  
225 230 235 240

Ser Asn Ala Val Ser Leu Thr Phe Asp Leu Ser Tyr Ile Thr Arg Leu  
245 250 255

50 Pro Pro Asp Leu Ser Arg Leu Val Pro Ser Ala Gly Phe Gln Ala Ala  
260 265 270

Ser Phe Pro Val Asp Val Ser Phe Thr Arg Asp Ser Thr Thr His Thr  
275 280 285

Tyr Gln Ala Tyr Gly Val Tyr Ser Ser Ser Arg Val Phe Thr Ile Thr  
290 295 300

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Arg Thr Gly Ile Asp Thr  
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<210> 9  
<211> 1617  
<212> DNA  
<213> Nelson Bay virus

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<223> CDS encoding P16 protein (SEQ ID NO:11)

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Ser Val Phe Gly Ser Val His Cys Gln Ser Ser Lys Asn Ser Ala Gly
   10          15          20          25

gga gat ctt cag gcg aca tcc gtt ttc acg acc tat tgg cca cat ttt      149
Gly Asp Leu Gln Ala Thr Ser Val Phe Thr Tyr Trp Pro His Phe
   30          35          40

40 gcc att ggt ggg ggt att ata gta gta atc ttg ttg ctt gga cta ttc      197
Ala Ile Gly Gly Ile Ile Val Val Ile Leu Leu Leu Gly Leu Phe
   45          50          55

tat tgc tgt tat ctt aag tgg aag aca tcc cag gtc aag cac acg tat      245
Tyr Cys Cys Tyr Leu Lys Trp Lys Thr Ser Gln Val Lys His Thr Tyr
   60          65          70

cgt cgt gag cta ata gcc ctt act cgt agt cat gtc cat tca acc cca      293
Arg Arg Glu Leu Ile Ala Leu Thr Arg Ser His Val His Ser Thr Pro
   75          80          85

50 tct ggt att tcg tat gtg tgagagttct ttttatgagc cttgggtgcg      341
Ser Gly Ile Ser Tyr Val
   90          95

atctggttac agatctgaga tttagttcat ttgccgtcg gaggtaacgt attatattaa      401
cgtgcacatt ccttagacc atccacaacg ttcaagtgcg tgcgcctctat ctccagacccc      461
cgttgctgg cacgtgtctt tgcttcgtcg tcgatcgatc gaccatcac ttccggatt      521
tttgtgagctt gactgtgtgc tgccggacat tcgatccaatc ccgagaagat tgggtctcg      581
agtttctcc tctcacgttg tcgttcaacta tgacagaacc actcagtcgg cagcagcgaa      641
aagagggtgt agccttgatt ttgacgtatca accagagcat aagcgcttcg cgatctgaca      701
tgagtgcgcg cggaaagcga gtgtctatca ttgaatcagc gcaggctgc ttacgtgtcg      761
atgttacttc ttgcagtcg gttagttccg gattgaattc caccatgcac gatctgtcag      821
cgtctgtcgc gaatctcaag actatcgta atactatgtc gtcaacagtt gccactatgg      881

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|  | tacagacaga | gctgagcaat   | gcgcaatctg | gattagcatc  | catgacgact | agttgtcaa   | 1001 |
|  | acttaacgac | tagtgtgaac   | gctaacgctg | tggccatatac | tggactaaa  | gcctcttta   | 1061 |
|  | actcactgtc | tagtcaatt    | cctacatcac | tcgcatactcc | cctgactgtc | tcaggcgta   | 1121 |
|  | tttaaagtct | gtctatgaat   | cgtaaattt  | gtggtgacgc  | tgctggttt  | aattcatatt  | 1181 |
|  | ccacattgtc | ccagatgcag   | tccttaact  | cgaatgttcc  | aacgtcatta | tctggtagcca | 1241 |
|  | atctgtccac | ttcttattctt  | gtgcattcgc | gtggtggtt   | gactgtattc | aatttgtcta  | 1301 |
|  | cgactcatgc | tttcacacacct | acgtcggtt  | atacccaaatt | gactatcgac | tgtcgaactt  | 1361 |
|  | ttaccccgtc | tccaaagtat   | tggtccgttc | taataccaaa  | accagcattt | caatcgagca  | 1421 |
|  | attttctgtg | tacgggttgg   | atgtgtgtca | acgacgcatt  | gatcccggca | agtgtgatcg  | 1481 |
|  | gtgcggtgga | tagtaatctt   | aaggtcatgt | tcttgcattt  | gactacgcgg | ccttcacagc  | 1541 |
|  | gaattacggg | cttggtcattc  | tatttcctta | tcgacacgtt  | gggggtggct | cccaccacta  | 1601 |
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<210> 10  
<211> 95  
<212> PRT  
<213> Nelson Bay virus

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Cys Gln Ser Ser Lys Asn Ser Ala Gly Gly Asp Leu Gln Ala Thr Ser  
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Val Phe Thr Thr Tyr Trp Pro His Phe Ala Ile Gly Gly Gly Ile Ile  
35 40 45

Val Val Ile Leu Leu Leu Gly Leu Phe Tyr Cys Cys Tyr Leu Lys Trp  
50 55 60

Lys Thr Ser Gln Val Lys His Thr Tyr Arg Arg Glu Leu Ile Ala Leu  
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Thr Arg Ser His Val His Ser Thr Pro Ser Gly Ile Ser Tyr Val  
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40 <210> 11  
<211> 140  
<212> PRT  
<213> Nelson Bay virus

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50 Tyr Glu Pro Trp Val Arg Ser Gly Tyr Arg Ser Glu Ile Ser Phe Ile  
20 25 30

Cys Arg Arg Glu Leu Thr Tyr Tyr Ile Asn Val His Ile Pro Leu Asp  
35 40 45

His Pro Gln Arg Ser Val Ala Cys Ala Leu Ser Gln Thr Pro Val Ala  
50 55 60

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 60 | Trp | His | Val | Ser | Leu | Leu | Arg | Arg | Arg | Ser | Tyr | Asp | Pro | Ser | Leu | Pro |
|    | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Asp Phe Cys Glu Leu Asp Cys Val Leu Arg His Ile Arg Pro Ile Pro  
                   85                         90                         95  
 Arg Arg Leu Val Ser Arg Gly Phe Ser Ser His Val Val Val His Tyr  
                   100                     105                         110  
 Asp Arg Thr Thr Gln Ser Pro Ala Ala Lys Arg Gly Cys Ser Leu Asp  
                   115                     120                         125  
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                   130                     135                     140  
  
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           20                     25                     30  
 Ala Leu Glu Lys Arg Val Ser Ile Ile Glu Ser Ala Gln Ala Ala Leu  
           35                     40                     45  
 30      Arg Val Asp Val Thr Ser Leu Gln Ser Val Ser Ser Gly Leu Asn Ser  
           50                     55                     60  
 Thr Met His Asp Leu Ser Ala Ser Val Ala Asn Leu Lys Thr Ile Val  
           65                     70                     75                 80  
 Asn Thr Met Ser Ser Thr Val Ala Thr Met Glu Gly Glu Leu Gln Ser  
           85                     90                     95  
 Cys Lys Ser Glu Ile Ser Asn Thr Gln Asn Val Leu Ser Val Val Gln  
           100                     105                     110  
 40      Thr Glu Leu Ser Asn Ala Gln Ser Gly Leu Ala Ser Met Thr Thr Ser  
           115                     120                     125  
 Leu Ser Asn Leu Thr Thr Ser Val Asn Ala Asn Ala Val Ala Ile Ser  
           130                     135                     140  
 Gly Leu Lys Ala Ser Leu Asn Ser Leu Ser Ser Ser Ile Pro Thr Ser  
           145                     150                     155                 160  
 50      Leu Ala Ser Pro Leu Thr Val Ser Gly Gly Ile Leu Ser Leu Ser Met  
           165                     170                     175  
 Asn Arg Lys Phe Cys Gly Asp Ala Ala Gly Leu Asn Ser Tyr Ser Thr  
           180                     185                     190  
 Leu Ser Gln Met Gln Ser Phe Asn Ser Asn Val Pro Thr Ser Leu Ser  
           195                     200                     205  
 60      Gly Thr Asn Leu Ser Thr Ser Ile Leu Val His Ser Arg Gly Gly Leu  
           210                     215                     220

|    |   |     |
|----|---|-----|
|    | Thr Val Phe Asn Leu Ser Thr Thr His Ala Phe Thr Pro Thr Ser Val |     |
|    | 225 230 235 240   |     |
|    | Asp Thr Lys Leu Thr Ile Asp Cys Arg Thr Phe Thr Pro Ser Pro Ser |     |
|    | 245 250 255   |     |
|    | Asp Trp Ser Val Leu Ile Pro Lys Pro Ala Phe Gln Ser Ser Asn Phe |     |
|    | 260 265 270   |     |
| 10 | Leu Cys Thr Gly Trp Met Cys Val Asn Asp Ala Trp Ile Pro Ala Ser |     |
|    | 275 280 285   |     |
|    | Val Ile Gly Ala Val Asp Ser Asn Pro Lys Val Met Phe Leu His Leu |     |
|    | 290 295 300   |     |
|    | Thr Thr Arg Pro Ser Gln Arg Ile Thr Gly Leu Val Ile Tyr Phe Ser |     |
|    | 305 310 315 320   |     |
|    | Ile Asp Thr   |     |
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|    | Met Gly Gln Arg His Ser Ile Val Gln                             |     |
| 40 | 1 5   |     |
|    | cca cca gct cca ccg cca aat gct ttt gtt gaa att gtg agc agt tct | 99  |
|    | Pro Pro Ala Pro Pro Asn Ala Phe Val Glu Ile Val Ser Ser Ser     |     |
|    | 10 15 20 25   |     |
|    | act ggc att ata atc gct gtt ggc ata ttt gca ttt ata ttc tca ttt | 147 |
|    | Thr Gly Ile Ile Ala Val Gly Ile Phe Ala Phe Ile Phe Ser Phe     |     |
|    | 30 35 40  |     |
| 50 | tta tat aag ttg ctg cag tgg tac aat cgt aag tca aag aat aag aaa | 195 |
|    | Leu Tyr Lys Leu Leu Gln Trp Tyr Asn Arg Lys Ser Lys Asn Lys Lys |     |
|    | 45 50 55  |     |
|    | cgt aaa gag caa att aga gaa caa att gag ctt ggt tta tta tca tat | 243 |
|    | Arg Lys Glu Gln Ile Arg Glu Gln Ile Glu Leu Gly Leu Leu Ser Tyr |     |
|    | 60 65 70  |     |
|    | ggt gct gga gta gca tca ctt cct ttg ctc aac gtt att gca cat aat | 291 |
|    | Gly Ala Gly Val Ala Ser Leu Pro Leu Leu Asn Val Ile Ala His Asn |     |
| 60 | 75 80 85  |     |

|    |  |             |
|----|--|-------------|
|    | cct gga tca gtt atc tcg gct acc cct atc tat aaa ggt ccg tgc act    | 339         |
|    | Pro Gly Ser Val Ile Ser Ala Thr Pro Ile Tyr Lys Gly Pro Cys Thr    |             |
|    | 90 95 100 105  |             |
|    | ggt gta cct aat tcg cgc cta ctt caa atc acg agc ggg act gca gaa    | 387         |
|    | Gly Val Pro Asn Ser Arg Leu Leu Gln Ile Thr Ser Gly Thr Ala Glu    |             |
|    | 110 115 120  |             |
| 10 | gag aac act aga att ttg aat cat gat gga aga aac cca gat gga agt    | 435         |
|    | Glu Asn Thr Arg Ile Leu Asn His Asp Gly Arg Asn Pro Asp Gly Ser    |             |
|    | 125 130 135  |             |
|    | atc aac gtt tgagtggcca aagtcattag atgaaaagttt gcaagtgtta           | 484         |
|    | Ile Asn Val  |             |
|    | 140  |             |
| 20 | tgtaatgagt tgaaggaaaa gactgaatgg caagatgaca tggaaagattg gatgccatac | 544         |
|    | tggatatata tggaaacatga tggattgct atctcgcaat ccagatactc actactccag  | 604         |
|    | caactagctg tatgggtgtg gaagtgcctc gactttgata tgggtgtgtca caatatctgg | 664         |
|    | acgacatggt tagtaaaaca tgcattgtct cgatgtcctg agttcgatga tgaggccttc  | 724         |
|    | tggctgggg tgcacaacaat tattaaatta gtaatttagga agacaatgca taggtacgct | 784         |
|    | tatcttgatg atagtaactct tgcggatttg actgagcagg ttggcctctg agttcattga | 844         |
|    | ccatgttagag actgcattgca cgcagcgcgg aaagtcattc atc                  | 887         |
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|    | Gly Ile Phe Ala Phe Ile Phe Ser Phe Leu Tyr Lys Leu Leu Gln Trp    | 35 40 45    |
| 40 | Tyr Asn Arg Lys Ser Lys Asn Lys Lys Arg Lys Glu Gln Ile Arg Glu    | 50 55 60    |
|    | Gln Ile Glu Leu Gly Leu Leu Ser Tyr Gly Ala Gly Val Ala Ser Leu    | 65 70 75 80 |
|    | Pro Leu Leu Asn Val Ile Ala His Asn Pro Gly Ser Val Ile Ser Ala    | 85 90 95    |
| 50 | Thr Pro Ile Tyr Lys Gly Pro Cys Thr Gly Val Pro Asn Ser Arg Leu    | 100 105 110 |
|    | Leu Gln Ile Thr Ser Gly Thr Ala Glu Glu Asn Thr Arg Ile Leu Asn    | 115 120 125 |
|    | His Asp Gly Arg Asn Pro Asp Gly Ser Ile Asn Val                    |             |
|    | 130 135 140  |             |
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|    | <211> 140  |             |

<212> PRT  
<213> baboon reovirus

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10 Glu Trp Gln Asp Asp Met Glu Asp Trp Met Pro Tyr Trp Ile Tyr Met  
35 40 45  
  
Lys His Asp Gly Ile Ala Ile Ser Gln Ser Arg Tyr Ser Leu Leu Gln  
50 55 60  
  
Gln Leu Ala Val Trp Val Trp Lys Cys Phe Asp Phe Asp Met Cys Val  
65 70 75 80  
  
20 Tyr Asn Ile Trp Thr Thr Trp Leu Val Lys His Ala Cys Ser Arg Cys  
85 90 95  
  
Pro Glu Phe Asp Asp Glu Ala Phe Trp Ser Gly Val Pro Thr Ile Ile  
100 105 110  
  
Lys Leu Val Ile Arg Lys Thr Met His Arg Tyr Ala Tyr Leu Asp Asp  
115 120 125  
  
30 Ser Thr Leu Ala Asp Leu Thr Glu Gln Val Gly Leu  
130 135 140